



SEQUENCE LISTING

<110> LITTLE, MELVYN
KIPRIYANOV, SERGEY
MOLDENHAUER, GERHARD
DEUTSCHES KREBSFORSCHUNGSZENTRUM

<120> MUTATED OKT3 ATIBODY

<130> 035280047US00

<140> 09/424,705

<141> 2000-06-02

<150> PCT/DE98/01409

<151> 1998-05-22

<160> 11

<170> FastSEQ for Windows Version 4.0

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<211> 909

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (28)...(900)

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gct ggc ttg ctg ctg ctg gca gct cag ccg gcc atg gcg cag gtg cag 102
Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln
10 15 20 25

ctg cag cag tct ggg gct gaa ctg gca aga cct ggg gcc tca gtg aag 150
Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys
30 35 40

atg tcc tgc aag gct tct ggc tac acc ttt act agg tac acg atg cac 198
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
45 50 55

tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att 246
Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile
60 65 70

aat cct agc cgt ggt tat act aat tac aat cag aag ttc aag gac aag 294
Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys
75 80 85

gcc aca ttg act aca gac aaa tcc tcc agc aca gcc tac atg caa ctg 342
Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu
90 95 100 105

agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca aga tat 390
Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr
110 115 120

tat gat gat cat tac agc ctt gac tac tgg ggc caa ggc acc act ctc 438
Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu
125 130 135

aca gtc tcc tca gcc aaa aca aca ccc aag ctt gaa gaa ggt gaa ttt 486
Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Glu Glu Gly Glu Phe
140 145 150

tca gaa gca cgc gta gat atc gtg ctc act cag tct cca gca atc atg 534
Ser Glu Ala Arg Val Asp Ile Val Leu Thr Gln Ser Pro Ala Ile Met
155 160 165

tct gca tct cca ggg gag aag gtc acc atg acc tgc agt gcc agc tca 582
Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser
170 175 180 185

agt gta agt tac atg aac tgg tac cag cag aag tca ggc acc tcc ccc 630
Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro
190 195 200

aaa aga tgg att tat gac aca tcc aaa ctg gct tct gga gtc cct gct 678
Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala
205 210 215

cac ttc agg ggc agt ggg tct ggg acc tct tac tct ctc aca atc agc 726
His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
220 225 230

ggc atg gag gct gaa gat gct gcc act tat tac tgc cag cag tgg agt 774
Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser
235 240 245

agt aac cca ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aac cgg 822
Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn Arg
250 255 260 265

gct gat act gca cca act gga tcc gaa caa aag ctg atc tca gaa gaa 870
Ala Asp Thr Ala Pro Thr Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu
270 275 280

gac cta aac tca cat cac cat cac cat cac taatctaga 909
Asp Leu Asn Ser His His His His His His
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<210> 2
<211> 291
<212> PRT
<213> Homo sapiens

INS
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D13

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 35 40 45
 Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
 50 55 60
 Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
 65 70 75 80
 Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys
 85 90 95
 Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
 100 105 110
 Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser Leu
 115 120 125
 Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr
 130 135 140
 Thr Pro Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg Val Asp Ile
 145 150 155 160
 Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
 165 170 175
 Val Thr Met Thr Cys Ser Ala Ser Ser Val Ser Tyr Met Asn Trp
 180 185 190
 Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr
 195 200 205
 Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser
 210 215 220
 Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala
 225 230 235 240
 Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly
 245 250 255
 Ser Gly Thr Lys Leu Glu Ile Asn Arg Ala Asp Thr Ala Pro Thr Gly
 260 265 270
 Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser His His His
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 His His His
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 <222> (28)...(897)

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 Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln

INS
E1
D13

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ctg cag cag tct ggg gct gaa ctg gca aga cct ggg gcc tca gtg aag Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys	30	35	40	150
atg tcc tgc aag gct tct ggc tac acc ttt act agg tac acg atg cac Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His	45	50	55	198
tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile	60	65	70	246
aat cct agc cgt ggt tat act aat tac aat cag aag ttc aag gac aag Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys	75	80	85	294
gac aag gcc aca ttg act aca gac aaa tcc tcc agc aca gcc tac atg Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met	90	95	100	342
caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala	110	115	120	390
aga tat tat gat gat cat tac agc ctt gac tac tgg ggc caa ggc acc Arg Tyr Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly Thr	125	130	135	438
act ctc aca gtc tcc tca gcc aaa aca aca ccc aag ctt ggc ggt gat Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly Asp	140	145	150	486
atc ttg ctc acc caa act cca gct tct ttg gct gtg tct cta ggg cag Ile Leu Leu Thr Gln Thr Pro Ala Ser Leu Ala Val Ser Leu Gly Gln	155	160	165	534
agg gcc acc atc tcc tgc aag gcc agc caa agt gtt gat tat gat ggt Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly	170	175	180	582
gat agt tat ttg aac tgg tac caa cag att cca gga cag cca ccc aaa Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys	190	195	200	630
ctc ctc atc tat gat gca tcc aat cta gtt tct ggg atc cca ccc agg Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg	205	210	215	678
ttt agt ggc agt ggg tct ggg aca gac ttc acc ctc aac atc cat cct Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro	220	225	230	726
gtg gag aag gtg gat gct gca acc tat cac tgt cag caa agt act gag Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu	235	240	245	774

gat ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa cgg gct 822
 Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala
 250 255 260 265

gat gct ggg gcc gct gga tcc gaa caa aag ctg atc tca gaa gaa gac 870
 Asp Ala Ala Ala Ala Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp
 270 275 280

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 Leu Asn Ser His His His His His His
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<210> 4
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 35 40 45
 Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly
 50 55 60
 Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr
 65 70 75 80
 Asn Tyr Asn Gln Lys Phe Lys Asp Lys Asp Lys Ala Thr Leu Thr Thr
 85 90 95
 Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser
 100 105 110
 Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr
 115 120 125
 Ser Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala
 130 135 140
 Lys Thr Thr Pro Lys Leu Gly Gly Asp Ile Leu Leu Thr Gln Thr Pro
 145 150 155 160
 Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
 165 170 175
 Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr
 180 185 190
 Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser
 195 200 205
 Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly
 210 215 220
 Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala
 225 230 235 240
 Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly
 245 250 255
 Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Ala Ala Gly Ser
 260 265 270
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser His His His His
 275 280 285
 His His

INS
 E1

D13

290

<210> 5

<211> 900

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (28)...(891)

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gct ggc ttg ctg ctg ctg gca gct cag ccg gcc atg gcg cag gtg cag 102

Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln

10

15

20

25

ctg cag cag tct ggg gct gag ctg gtg agg cct ggg tcc tca gtg aag 150

Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys

30

35

40

att tcc tgc aag gct tct ggc tat gca ttc agt agc tac tgg atg aac 198

Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn

45

50

55

tgg gtg aag cag agg cct gga cag ggt ctt gag tgg att gga cag att 246

Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile

60

65

70

tgg cct gga gat ggt gat act aac tac aat gga aag ttc aag ggt aaa 294

Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys

75

80

85

gcc act ctg act gca gac gaa tcc tcc agc aca gcc tac atg caa ctc 342

Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu

90

95

100

105

agc agc cta gca tct gag gac tct gcg gtc tat ttc tgt gca aga cgg 390

Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg

110

115

120

gag act acg acg gta ggc cgt tat tac tat gct atg gac tac tgg ggt 438

Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly

125

130

135

caa gga acc tca gtc acc gtc tcc tca gcc aaa aca aca ccc aag ctt 486

Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu

140

145

150

ggc ggt gat atc gtg ctc act cag tct cca gca atc atg tct gca tct 534

Gly Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser

155

160

165

cca ggg gag aag gtc acc atg acc tgc agt gcc agc tca agt gta agt 582

INS
EI

D13

Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser
 170 175 180 185

tac atg aac tgg tac cag cag aag tca ggc acc tcc ccc aaa aga tgg 630
 Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp
 190 195 200

att tat gac aca tcc aaa ctg gct tct gga gtc cct gct cac ttc agg 678
 Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg
 205 210 215

ggc agt ggg tct ggg acc tct tac tct ctc aca atc agc ggc atg gag 726
 Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu
 220 225 230

gct gaa gat gct gcc act tat tac tgc cag cag tgg agt agt aac cca 774
 Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro
 235 240 245

ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aac cgg gct gat act 822
 Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn Arg Ala Asp Thr
 250 255 260 265

gca cca act gga tcc gaa caa aag ctg atc tca gaa gaa gac cta aac 870
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 270 275 280

tca cat cac cat cac cat cac taatctaga 900
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<210> 6
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 <213> Homo sapiens

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 20 25 30
 Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
 35 40 45
 Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly
 50 55 60
 Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr
 65 70 75 80
 Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu
 85 90 95
 Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp
 100 105 110
 Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg
 115 120 125
 Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
 130 135 140
 Ser Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly Asp Ile Val Leu Thr

ANS
 EI

D13

145 150 155 160
 Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met
 165 170 175
 Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln
 180 185 190
 Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu
 195 200 205
 Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser
 210 215 220
 Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr
 225 230 235 240
 Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr
 245 250 255
 Lys Leu Glu Ile Asn Arg Ala Asp Thr Ala Pro Thr Gly Ser Glu Gln
 260 265 270
 Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser His His His His His His
 275 280 285

<210> 7
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<400> 7
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24

<210> 8
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<400> 8
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32

<210> 9
 <211> 32
 <212> DNA
 <213> Homo sapiens

<400> 9
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32

<210> 10
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 <212> DNA
 <213> Homo sapiens

<400> 10
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48

<210> 11
 <211> 48
 <212> DNA
 <213> Homo sapiens

<400> 11
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48

INS
EI

D13